

RESULT 1
US-09-818-780-89
; Sequence 89, Application US/09818780
; Patent No. 6677146
; GENERAL INFORMATION:
; APPLICANT: McHenry, Charles
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III HOLOENZYME
; FILE REFERENCE: 1794.0030004
; CURRENT APPLICATION NUMBER: US/09/818, 780
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192, 736
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-09-818-780-89

Query Match 100.0%; Score 1570; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 7.6e-142;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVFLEKLQKTLHIPGGLFYGKEGSGKTAKTAFAKGILCKENVPWGCGSCPSCKHVN 60
|||
Db 1 MEKVFLEKLQKTLHIPGGLFYGKEGSGKTAKTAFAKGILCKENVPWGCGSCPSCKHVN 60

Qy 61 ELEEAFFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120
|||
Db 61 ELEEAFFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120

Qy 121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILTTNRRSAILPTILSRTFQV 180
|||
Db 121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILTTNRRSAILPTILSRTFQV 180

Qy 181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLAS 240
|||
Db 181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLAS 240

Qy 241 EFEKWEPEKQKLFLEIMEELVSQKLTEKKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL 300
|||
Db 241 EFEKWEPEKQKLFLEIMEELVSQKLTEKKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL 300

Qy 301 AVQAD 305
|||
Db 301 AVQAD 305

RESULT 1
D70432
conserved hypothetical protein aq_1526 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: D70432

R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70432
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-305
A;Cross-references: UNIPROT:067486; UNIPARC:UPI00004350C; GB:AE000744; NID:g2983891; PIDN: AAC07454.1; PID:g2983903; GB:AE000657
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1526

RESULT 1

067486 AQUAE

ID 067486_AQUAE PRELIMINARY; PRT; 305 AA.

AC 067486 ;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein aq_1526.

GN OrderedLocusNames=AQ_1526;

OS *Aquifex aeolicus.*

OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.

OX NCBI_TaxID=63363;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium *Aquifex*
 RT *aeolicus*";
 RL Nature 392:353-358(1998).
 DR EMBL; AE000744; AAC07454.1; -; Genomic_DNA.
 DR PIR; D70432; D70432.
 DR HSSP; P06710; 1NJF.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR SMART; SM00382; AAA; 1.
 KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
 SQ SEQUENCE 305 AA; 34897 MW; 2B207935455B7E8A CRC64;

Query Match 100.0%; Score 1570; DB 2; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.5e-91;
 Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEKVFLEKLQKTLHIPGGLLFYGKEGSGKTAKAFAKGILCKENVPWGCSCPCKHVN 60
Db	1 MEKVFLEKLQKTLHIPGGLLFYGKEGSGKTAKAFAKGILCKENVPWGCSCPCKHVN 60

Qy	61 ELEEAFFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120
Db	61 ELEEAFFKGEIEDFKVYKDKDGKKHFVYLMGEHPDFVVIIPSGHYIKIEQIREVKNFAYV 120

Qy	121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILTTNRRSAILPTILSRTFQV 180
Db	121 KPALSRRKVIIIDDAHAMTSQAANALLKVLEEPPADTTFILTTNRRSAILPTILSRTFQV 180

Qy	181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLAS 240
Db	181 EFKGFSVKEVMEIAKVDEEIAKLSGGSLKRAILLKENKDILNKVKEFLENEPLKVYKLAS 240

Qy	241 EFEKWEPEKQKLFLEIMEELVSQKLTEEKKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL 300
Db	241 EFEKWEPEKQKLFLEIMEELVSQKLTEEKKDNYTYLLDTIRLFKDGLARGVNEPLWLFTL 300

Qy	301 AVQAD 305
Db	301 AVQAD 305

STN SEARCH:

(FILE 'HOME' ENTERED AT 14:57:48 ON 01 DEC 2008)

FILE 'MEDLINE, CAPLUS, SCISEARCH, BIOTECHNO, EMBASE, JAPIO' ENTERED AT
15:00:53 ON 01 DEC 2008

L1 217 S AQUIFEX AND POLYMERASE

L2 110 DUP REM L1 (107 DUPLICATES REMOVED)

L3 9 S L2 AND DELTA